

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/784,633A  
Source: 1FW0  
Date Processed by STIC: 10/18/04

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DATE: 10/18/2004

PATENT APPLICATION: US/10/784,633A

TIME: 10:01:23

Input Set : A:\pto.pg.txt

Output Set: N:\CRF4\09282004\J784633A.raw

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3 <110> APPLICANT: SHIRAI, Tomoyuki
4     ASAMOTO, Makoto
5     HOKAIWADO, Naomi
7 <120> TITLE OF INVENTION: Carcinogen-hypersensitive rat
9 <130> FILE REFERENCE: 671302-3004
11 <140> CURRENT APPLICATION NUMBER: 10/784,633A
12 <141> CURRENT FILING DATE: 2004-02-23
14 <150> PRIOR APPLICATION NUMBER: JP P2001-253241
15 <151> PRIOR FILING DATE: 2001-08-23
17 <150> PRIOR APPLICATION NUMBER: JP 2001-253241
18 <151> PRIOR FILING DATE: 2001-08-23
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1485
26 <212> TYPE: DNA
27 <213> ORGANISM: Rattus norvegicus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (32)..(883)
33 <400> SEQUENCE: 1
34 cgcagtgcca gggagggtgtg aatgaggcag g atg aac tgg aca ggt cta tac      52
35                               Met Asn Trp Thr Gly Leu Tyr
36                               1           5
38 acc ttg ctc agt ggc gtg aat cgg cat tct aca gcc att ggc cga gta      100
39 Thr Leu Leu Ser Gly Val Asn Arg His Ser Thr Ala Ile Gly Arg Val
40         10           15           20
42 tgg ctg tcc gtc atc ttt atc ttc aga atc atg gtg ctg gtg gtg gct      148
43 Trp Leu Ser Val Ile Phe Ile Phe Arg Ile Met Val Leu Val Val Ala
44         25           30           35
46 gca gag agc gtg tgg ggt gat gag aag tct tct ttc atc tgt aac acc      196
47 Ala Glu Ser Val Trp Gly Asp Glu Lys Ser Ser Phe Ile Cys Asn Thr
48 40           45           50           55
50 ctc cag ccg ggc tgt aac agc gtc tgc tat gac cat ttt ttc ccc atc      244
51 Leu Gln Pro Gly Cys Asn Ser Val Cys Tyr Asp His Phe Phe Pro Ile
52         60           65           70
54 tcc cat gtg cgc ctg tgg tcc ctg caa ctc atc ttg gtt tcc acc cca      292
55 Ser His Val Arg Leu Trp Ser Leu Gln Leu Ile Leu Val Ser Thr Pro
56         75           80           85
58 gct ctc ctc gtg gca atg cac gtg gct cac caa caa cac ata gaa aag      340
59 Ala Leu Leu Val Ala Met His Val Ala His Gln Gln His Ile Glu Lys
60         90           95           100
62 aaa atg cta cgg ctt gag ggg cac ggg gac ccc ctt cac ctg gaa gag      388

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63 Lys Met Leu Arg Leu Glu Gly His Gly Asp Pro Leu His Leu Glu Glu
64      105                      110                      115
66 gta aag agg cac aag gtg cac atc tca ggg aca ctg tgg tgg acc tat 436
67 Val Lys Arg His Lys Val His Ile Ser Gly Thr Leu Trp Trp Thr Tyr
68 120                      125                      130                      135
70 gtc atc agt gtg gtg ttc cgg ctg ctg ttt gag gct gtc ttc atg tat 484
71 Val Ile Ser Val Val Phe Arg Leu Leu Phe Glu Ala Val Phe Met Tyr
72                      140                      145                      150
74 gtc ttc tat ctg ctc tac ccg ggc tat gcc atg gtg cgg ctg gtc aag 532
75 Val Phe Tyr Leu Leu Tyr Pro Gly Tyr Ala Met Val Arg Leu Val Lys
76                      155                      160                      165
78 tgt gag gcc ttc ccc tgc ccc aac acg gtg gac tgc ttc gtg tcc cgc 580
79 Cys Glu Ala Phe Pro Cys Pro Asn Thr Val Asp Cys Phe Val Ser Arg
80                      170                      175                      180
82 ccc act gag aaa acc gtc ttc act gtc ttt atg ctc gcc gcc tcc ggc 628
83 Pro Thr Glu Lys Thr Val Phe Thr Val Phe Met Leu Ala Ala Ser Gly
84                      185                      190                      195
86 atc tgc att atc ctc aac gtg gcg gag gtg gtg tac ctc atc atc cgg 676
87 Ile Cys Ile Ile Leu Asn Val Ala Glu Val Val Tyr Leu Ile Ile Arg
88 200                      205                      210                      215
90 gcc tgt gcc cgc cgt gct cag cgc cgc tcc aat ccg ccc tcc cgc aag 724
91 Ala Cys Ala Arg Arg Ala Gln Arg Arg Ser Asn Pro Pro Ser Arg Lys
92                      220                      225                      230
94 ggc tgc gcc ttc gcc cac cgc ctc tca cct gaa tac aag cag aat gag 772
95 Gly Ser Gly Phe Gly His Arg Leu Ser Pro Glu Tyr Lys Gln Asn Glu
96                      235                      240                      245
98 atc aac aag ctg ctg agc gag cag gat ggc tct ctg aaa gac ata ctg 820
99 Ile Asn Lys Leu Leu Ser Glu Gln Asp Gly Ser Leu Lys Asp Ile Leu
100                      250                      255                      260
102 cgc cgc agt cct gcc act ggg gcc ggg ctg gct gag aag agc gac cga 868
103 Arg Arg Ser Pro Gly Thr Gly Ala Gly Leu Ala Glu Lys Ser Asp Arg
104                      265                      270                      275
106 tgc tca gcc tgc tga tgccgagtac caggcaacct cccatccaac ccctccctca 923
107 Cys Ser Ala Cys
108 280
110 cccacccag gcctgccct ccttctccta tgctggtgag caggcctctg cctcctaggg 983
112 attactccat caaaccttcc ctccctccct actccccttc ctcagagagt cttctgtcaa 1043
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118 agatgttctg aaggtgtttc caattaggaa acgtaatctt aacccccatg ctgtcaggta 1223
120 cccactttg ggagtcatgt cagtggggag ggctgtgagc aagcagagtg gaggaggggc 1283
122 tctgcactgt ggatggagaa gggaggggag cttgccttgc tgctgtctac aaggaaaagg 1343
124 aggacacatc taggggtggg gagttctgga gggagaagca ggcagataaa tcagagtggg 1403
126 ggttggtcag ggctgcccc agtccccagt tcccaaggcc tctctctctg aaaatgttac 1463
128 acattaaaca ggattttaca gt 1485
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 283
133 <212> TYPE: PRT
134 <213> ORGANISM: Rattus norvegicus

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136 &lt;400&gt; SEQUENCE: 2

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137 Met Asn Trp Thr Gly Leu Tyr Thr Leu Leu Ser Gly Val Asn Arg His
138   1           5           10           15
139 Ser Thr Ala Ile Gly Arg Val Trp Leu Ser Val Ile Phe Ile Phe Arg
140           20           25           30
141 Ile Met Val Leu Val Val Ala Ala Glu Ser Val Trp Gly Asp Glu Lys
142           35           40           45
143 Ser Ser Phe Ile Cys Asn Thr Leu Gln Pro Gly Cys Asn Ser Val Cys
144           50           55           60
145 Tyr Asp His Phe Phe Pro Ile Ser His Val Arg Leu Trp Ser Leu Gln
146           65           70           75           80
147 Leu Ile Leu Val Ser Thr Pro Ala Leu Leu Val Ala Met His Val Ala
148           85           90           95
149 His Gln Gln His Ile Glu Lys Lys Met Leu Arg Leu Glu Gly His Gly
150           100          105          110
151 Asp Pro Leu His Leu Glu Glu Val Lys Arg His Lys Val His Ile Ser
152           115          120          125
153 Gly Thr Leu Trp Trp Thr Tyr Val Ile Ser Val Val Phe Arg Leu Leu
154           130          135          140
155 Phe Glu Ala Val Phe Met Tyr Val Phe Tyr Leu Leu Tyr Pro Gly Tyr
156           145          150          155          160
157 Ala Met Val Arg Leu Val Lys Cys Glu Ala Phe Pro Cys Pro Asn Thr
158           165          170          175
159 Val Asp Cys Phe Val Ser Arg Pro Thr Glu Lys Thr Val Phe Thr Val
160           180          185          190
161 Phe Met Leu Ala Ala Ser Gly Ile Cys Ile Ile Leu Asn Val Ala Glu
162           195          200          205
163 Val Val Tyr Leu Ile Ile Arg Ala Cys Ala Arg Arg Ala Gln Arg Arg
164           210          215          220
165 Ser Asn Pro Pro Ser Arg Lys Gly Ser Gly Phe Gly His Arg Leu Ser
166           225          230          235          240
167 Pro Glu Tyr Lys Gln Asn Glu Ile Asn Lys Leu Leu Ser Glu Gln Asp
168           245          250          255
169 Gly Ser Leu Lys Asp Ile Leu Arg Arg Ser Pro Gly Thr Gly Ala Gly
170           260          265          270
171 Leu Ala Glu Lys Ser Asp Arg Cys Ser Ala Cys
172           275          280

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176 &lt;210&gt; SEQ ID NO: 3

177 &lt;211&gt; LENGTH: 21

178 &lt;212&gt; TYPE: DNA

179 &lt;213&gt; ORGANISM: Artificial Sequence

181 &lt;220&gt; FEATURE:

182 <223> OTHER INFORMATION: Artificial insertion sequence obtained from  
digestion of a plasmid

183 moiety

185 &lt;400&gt; SEQUENCE: 3

186 catcatcacc atcaccattg a

21

189 &lt;210&gt; SEQ ID NO: 4

190 &lt;211&gt; LENGTH: 20

191 &lt;212&gt; TYPE: DNA

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192 <213> ORGANISM: Artificial Sequence  
194 <220> FEATURE:  
195 <223> OTHER INFORMATION: PCR primer P1  
197 <400> SEQUENCE: 4  
198 aacgtggcgc aggtggtgta 20  
201 <210> SEQ ID NO: 5  
202 <211> LENGTH: 20  
203 <212> TYPE: DNA  
204 <213> ORGANISM: Artificial Sequence  
206 <220> FEATURE:  
207 <223> OTHER INFORMATION: PCR Primer P2  
209 <400> SEQUENCE: 5  
210 atggtgatgg tgatgatggc 20  
213 <210> SEQ ID NO: 6  
214 <211> LENGTH: 21  
215 <212> TYPE: DNA  
216 <213> ORGANISM: Artificial Sequence  
218 <220> FEATURE:  
219 <223> OTHER INFORMATION: PCR Primer P3  
221 <400> SEQUENCE: 6  
222 ggaaggttt gatggagtaa t 21

**VERIFICATION SUMMARY**

DATE: 10/18/2004

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